**Evolutionary Genetics - Snail Report**

Polymorphism can be defined as the recurrence within a population of two or more discontinuous genetic variants of a specific trait in such proportions that they cannot be maintained simply by mutation. (Mosby, 2009). There are at least 8 evolutionary forces that are now known to affect the shell polymorphism in *C. nemoralis*, suggesting that the genetic structure of each *Cepaea* population requires a complex explanation, and cannot be explained just by one factor (Jones et al, 1977). Mutation can account or the origin of the polymorphism. Genetic drift and/or natural selection can explain the spread or loss of the polymorphism, and gene flow explains how the polymorphism moves from one habitat to another. Other explanations also include bottleneck and pseudoreplication.

*Cepaea nemoralis* are also known as the grove snail, or brown lipped snail, have been used repeatedly to explain the factors behind polymorphism. This is due to the fact that they display their genotypes on their shells. They are also easy to study due to their slow migration, making it possible to study a large sample in a single field. *Cepaea* are polymorphic for colour and number of black bands on their shells, amongst other features. There are two pairs of *Cepaea* species within this genus; *C. nemoralis* and *C. hortensis,* and *C. vindobonensis* and *C. sylvatica.* This study looked at C. nemoralis.

Our investigation aims to identify whether natural selection accounts for the polymorphism in the species *C. nemoralis,* or if the differences are due to genetic drift. For example, if the results show that the colour of the snails matches the environment they live in, this could suggest the involvement of natural selection. However, it is important to consider the possibility of pseudo-replication and population bottleneck, which could also explain these observations. If the shell colours tend not to match the environment the snails live in, this could suggest that the polymorphism is a result of random gene flow processes such as genetic drift, and not selection.

To test this, we designed our experiment to include 6 samples, which were 3 pairs of 2 distributed horizontally across a field, with one pair (Pair 3) being further away than the first 2. The reason for this is to minimise the chances of pseudo-replication. The study controlled for habitat by only sampling bushes. Having our samples in pairs ensures some form of replication, while having 3 different pairs allows for comparison between the samples.

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